AMENDMENTS TO THE CLAIMS

The following list of claims will replace all prior versions and lists of claims in the application.

Listing of Claims:

1. (Currently amended) A method for diagnosis of renal cell carcinoma (RCC), the method comprising the steps of:

(a) providing at least one peripheral blood sample of a human; ~~and~~

(b) generating ~~comparing~~ an expression profile comprising expression levels of one or more RCC disease genes in said at least one peripheral blood sample;

(c) comparing the expression profile generated in step (b) to at least one reference expression profile comprising expression levels of said one or more RCC disease genes, wherein the comparison ~~the difference or similarity between the expression profile and the at least one reference expression profile of said one or more RCC disease genes~~ is indicative of the presence or absence of RCC in the human, and

wherein said one or more RCC disease genes are selected from the group consisting of: eukaryotic elongation factor 1 alpha 2 (EEF1A2); toll-like receptor 2 (TLR2); zinc finger protein 36, C3H type-like 2 (BRF2); lectin, galactoside-binding, soluble, 3 (LGALS3); small nuclear ribonucleoprotein polypeptide G (SNRPG); Ras-induced senescence 1 (DKFZP586E1621); nuclear mitotic apparatus protein 1 (NUMA1); superoxide dismutase 2 (SOD2); aldo-keto reductase family 1, member B1 (AKR1B1); dual specificity phosphatase 6 (DUSP6); SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily e, member 1 (SMARCE1); KIAA0669; MLL septin-like fusion (MSF); interleukin 1 receptor antagonist (IL1RN); prothymosin, alpha (PTMA); KIAA0410; proteasome 26S subunit, non-ATPase, 3 (PSMD3); T54 protein (T54); complement component 1, q subcomponent binding protein (C1QBP); and oxidative-stress responsive 1 (OSR1) ~~one gene selected from Table 4 or Table 6, provided that if said one or more RCC disease genes consist of only one gene, said one gene is not selected from the group consisting of IL1B, IL6, MMP-9 and FCGR3B, and further provided that if said one or more RCC disease genes consist of two genes, said two genes are not IL1B and IL6~~.

2. (Canceled)

3. (Previously presented) The method according to claim 1, wherein said peripheral blood sample comprises enriched peripheral blood mononuclear cells (PBMCs).

4. (Previously presented) The method according to claim 1, wherein said peripheral blood sample is a whole blood sample.

5. (Currently amended) The method according to claim 1, wherein the expression profile generated in step (b) is ~~determined~~ generated using quantitative RT-PCR or an immunoassay.

6. (Currently amended) The method according to claim 1, wherein said at least one reference expression profile comprises ~~an~~ reference expression profile comprising expression levels of said one or more RCC disease genes in peripheral blood samples of disease-free humans.

7. (Currently amended) The method according to claim 6, wherein said at least one reference expression profile further comprises ~~an~~ reference expression profile comprising expression levels of said one or more RCC disease genes in peripheral blood samples of patients having RCC.

8. (Currently amended) The method according to claim 7, wherein said one or more RCC disease genes include at least two genes, and the expression profile generated in step (b) is compared to said at least one reference expression profile using a weighted voting algorithm.

9-20. (Canceled)

21. (New) The method according to claim 1, wherein said one or more RCC disease genes are TLR2 and EEF1A2.

22. (New) The method according to claim 1, wherein said one or more RCC disease genes are TLR2, LGALS3, EEF1A2, and BRF2.

23. (New) The method according to claim 1, wherein said one or more RCC disease genes are TLR2, LGALS3, DKFZP586E1621, EEF1A2, BRF2, and SNRPG.

24. (New) The method according to claim 1, wherein said one or more RCC disease genes are TLR2, LGALS3, DKFZP586E1621, SOD2, EEF1A2, BRF2, SNRPG, and NUMA1.

25. (New) The method according to claim 1, wherein said one or more RCC disease genes are TLR2, LGALS3, DKFZP586E1621, SOD2, DUSP6, EEF1A2, BRF2, SNRPG, NUMA1, and AKR1B1.

26. (New) The method according to claim 1, wherein said one or more RCC disease genes are TLR2, LGALS3, DKFZP586E1621, SOD2, DUSP6, KIAA0669, EEF1A2, BRF2, SNRPG, NUMA1, AKR1B1, and SMARCE1.

27. (New) The method according to claim 1, wherein said one or more RCC disease genes are TLR2, LGALS3, DKFZP586E1621, SOD2, DUSP6, KIAA0669, IL1RN, EEF1A2, BRF2, SNRPG, NUMA1, AKR1B1, SMARCE1, and MSF.

28. (New) The method according to claim 1, wherein said one or more RCC disease genes are TLR2, LGALS3, DKFZP586E1621, SOD2, DUSP6, KIAA0669, IL1RN, KIAA0410, EEF1A2, BRF2, SNRPG, NUMA1, AKR1B1, SMARCE1, MSF, and PTMA.

29. (New) The method according to claim 1, wherein said one or more RCC disease genes are TLR2, LGALS3, DKFZP586E1621, SOD2, DUSP6, KIAA0669, IL1RN, KIAA0410, T54, EEF1A2, BRF2, SNRPG, NUMA1, AKR1B1, SMARCE1, MSF, PTMA, and PSMD3.

30. (New) The method according to claim 1, wherein said one or more RCC disease genes are EEF1A2, TLR2, BRF2, LGALS3, SNRPG, DKFZP586E1621, NUMA1, SOD2, AKR1B1, DUSP6, SMARCE1, KIAA0669, MSF, IL1RN, PTMA, KIAA0410, PSMD3, T54, C1QBP, and OSR1.